

31 ATGGCCAACAAGCTGAGGAAATCGAACGCCATCGAATGGGCCACGGCCACGGCACAGTACCGCTCCTGGAAAGGAGCTGCTGCCACAGC
 1 M A N K L R K S N A I E W A T A T G T V P L L E R S C C H S

91 GAGGACGCCGCACTGGAGCCCCAAGCGAGCAAAACCAGCCATAGAGAACAAGCCCCCATCTGCGCCACCTGAGCCAACTGAGCCACCTG
 31 E D A A L E P Q A S K T S H R E Q A P I L R H L S Q L S H L

181 CTCATCATCGCCGACTGCTGATCGTCTGCTTGGCGGGCGTGACGGAGGGCCCGGCATGCGCCGCTCATGTTGAGGAGTCCGACACG
 61 L I I A G L L I V C L A G V T E G R R H A P L M F E E S D T

271 GGCAGGCGGTCCAACCGACCGGTCAACGAATGCCAGTTTGGCAAAGTTTGGCGCAATTGGGGTCCACCTGGTATGCGGATTTGGGT
 91 G R R S N R P A V T E C Q F G K V L R E L G S T W Y A D L G

361 CCACCTTCGGAGTTATGTACTGCATCAAGTGTGAATGTGTGCGCATACCCAAGAAGCGGCGCATCGTTGCACGCGTCCAGTGTGCGCAAT
 121 P P F G V M Y C I K C E C V A I P K K R R I V A R V Q C R N

451 ATCAAAAACGAGTGCCCGCCGGCCAAATGCGATGATCCCATCTCGTTGCCCCGAAAATGCTGCAAGACCTGTCCCGCGATCGAAACGAT
 151 I K N E C P P A K C D D P I S L P G K C C K T C P G D R N D

541 ACGGATGTAGCCTTGATGTGCCGTGCCCAATGAAGAGGAAGAGCGCAACATGAACATTACGCTGCGTTGCTAACGGGCCGACCTCC
 181 T D V A L D V P V P N E E E E R N M K H Y A A L L T G R T S

631 TATTTCTCAAGGGTGAGGAAATGAAGTCCATGTACACCACCTACAATCCGAGAATCTGGTGGCCACCGCCGTTTCTGTTCCACAAG
 211 Y F L K G E E M K S M Y T T Y N P Q N V V A T A R F L F H K

721 AAGAATCTATACTACTCTTCTACACCTCATCGGAATCGGTGTCGCGTGCCATTCAATTCGTTGATGATGCGGGTGTAACTCCTGGAG
 241 K N L Y Y S F Y T S S R I G R P R A I Q F V D D A G V I L E

811 GAGCATCAACTGGAGACCACCTTGGCGGGCACTCTCAGTGTCTATCAGAATGCCACGGGCAAGATCTGA
 271 E H Q L E T T L A G T L S V Y A N A T G K I STOP

* * *

TM

CR1

FIGURE 1

1 ATGGCCAACAAGCTGAGGAAATCGAACGCCATCGAATGGGCCACGGCCACCGGCACAGTACCGCTCCTGGAAAGGAGCTGCTGCCACAGC
 1 M A N K L R K S N A I E W A T A T G T V P L L E R S C C H S

91 GAGGACGCCGCACTGGAGCCCCAAGCGAGCAAAACCAGCCATAGAGAACAAGCCCCCATCCTGCGCCACCTGAGCCAACCTGAGCCACCTG TM
 31 E D A A L E P Q A S K T S H R E Q A P I L R , H L S , Q L S H L

181 CTCATCATCGCCGACTGCTGATCGTCTGCTTGGCGGGCGTGACGGAGGGCCGCGCATGCGCCGCTCATGTTGAGGAGTCCGACACG
 61 L I I A G L L I V C L A G V T E G R R H A P L M F E E S D T

271 GGCAGGCGGTCCAACCGACCGGTACCGAATGCCAGTTTGGCAAAGTTTGGCGGAATTGGGGTCCACCTGGTATGCGGATTTGGGT
 91 G R R S N R P A V T E C Q F G K V L R E L G S T W Y A D L G

361 CCACCCTTCGGAGTTATGTACTGCATCAAGTGTGAATGTGTGCGCATACCCAAGAAGCGGCGCATCGTTGCACGCGTCCAGTGTGCGCAAT
 121 P P F G V M Y C I K C E C V A I P K K R R I V A R V Q C R N } CRI

451 ATCAAAAACGAGTGCCCGCCGCCAAATGCGATGATCCCATCTCGTTGCCCGGAAAATGCTGCAAGACCTGTCCCGCGATCGAAACGAT
 151 I K N E C P P A K C D D P I S L P G K C C K T C P G D R N D * *

541 ACGGATGTAGCCTTGGATGTGCCCGTGCCCAATGAAGAGGAAGAGCGCAACATGAAACATTACGCTGCGTTGCTAACGGGCCGCACCTCC
 181 T D V A L D V P V P N E E E E R N M K H Y A A L L T G R T S *

631 TATTTCTCAAGGGTGAGGAAATGAAGTCCATGTACACCACCTACAATCCGAGAATCTGGTGGCCACCGCCGTTTCTGTTCCACAAG
 211 Y F L K G E E M K S M Y T T Y N P Q N V V A T A R F L F H K

721 AAGAATCTATACTACTCTTCTACACCTCATCGGAATCGGTGTCGCGTGCCATTCAATTCGTTGATGATGCGGGTGTAACTCCTGGAG
 241 K N L Y Y S F Y T S S R I G R P R A I Q F V D D A G V I L E

811 GAGCATCAACTGGAGACCACCTTGGCGGGCACTCTCAGTGTCTATCAGAATGCCACGGGCAAGATCGGCCGCGGCTCGAGGGTACCTCTA
 271 E H Q L E T T L A G T L S V Y A N A T G K I G R G S R V P L } pUAS
 * * * Sequences

901 GAGGATCTTTCTGAAGGAACCTTACTTCTGTCGTGTGACATAATTGGACAACTACCTACAGAGATTTAAAGCTCTAA
 301 E D L C E G T L L L W C D I I G N T T Y R D L K L STOP

FIGURE 2

1 ATGGCCAACAAGCTGAGGAAATCGAACGCCATCGAATGGGCCACGGCCACCGGCACAGTACCGCTCCTGGAAGGAGCTGCTGCCACAGC
 1 M A N K L R K S N A I E W A T A T G T V P L L E R S C C H S

91 GAGGACGCCGCACTGGAGCCCCAAGCGAGCAAAACCAGCCATAGAGAACAAGCCCCCATCCTGCGCCACCTGAGCCAACTGAGCCACCTG TM
 31 E D A A L E P Q A S K T S H R E Q A P I L R H L S Q L S H L

181 CTCATCATCGCCGACTGCTGATCGTCTGCTTGGCGGGCGTGACGGAGGGCCGCGCATGCGCCGCTCATGTTGAGGAGTCCGACACG
 61 L I I A G L L I V C L A G V T E G R R H A P L M F E E S D T

271 GGCAGGCGGTCCAACCGACCGGTCAACGAATGCCAGTTTGGCAAAGTTTGGCGGAATTGGGGTCCACCTGGTATGCGGATTGGGT
 91 G R R S N R P A V T E C Q F G K V L R E L G S T W Y A D L G

361 CCACCCTTCGGAGTTATGTACTGCATCAAGTGTGAATGTGTGCGCATACCCAAGAAGCGGCGCATCGTTGACCGCTCCAGTGTGCGCAAT
 121 P P F G V M Y C I K C E C V A I P K K R R I V A R V Q C R N CR1:W->A

451 ATCAAAAACGAGTGCCCGCCGCCAAATGCGATGATCCCATCTCGTTGCCCGGAAAAATGCTGCAAGACCTGTCCCGGCGATCGAAACGAT
 151 I K N E C P P A K C D D P I S L P G K C C K T C P G D R N D *

541 ACGGATGTAGCCTTGGATGTGCCCGTGCCCAATGAAGAGGAAGAGCGCAACATGAAACATTACGCTGCGTTGCTAACGGGCCGACCTCC
 181 T D V A L D V P V P N E E E E R N M K H Y A A L L T G R T S *

631 TATTTCTCAAGGGTGAGGAAATGAAGTCCATGTACACCACCTACAATCCGAGAATCTGGTGGCCACCGCCCGTTTCTGTTCCACAAG
 211 Y F L K G E E M K S M Y T T Y N P Q N V V A T A R F L F H K

721 AAGAATCTATACTACTCTTCTACACCTCATCGGAATCGGTGTCGCGTGCCATTCAATTCGTTGATGATGCGGGTGTAACTCCTGGAG
 241 K N L Y Y S F Y T S S R I G R P R A I Q F V D D A G V I L E

811 GAGCATCAACTGGAGACCACCTTGGCGGGCACTCTCAGTGTCTATCAGAATGCCACGGGCAAGATCGGCCGCGGCTCGAGGGTACCTCTA
 271 E H Q L E T T L A G T L S V Y A N A T G K I G R G S R V P L * * *

901 GAGGATCTTTGTGAAGGAACCTTACTTCTGTGGTGTGACATAATTGGACAACTACCTACAGAGATTAAAGCTCTAA
 301 E D L C E G T L L L W C D I I G N T T Y R D L K L STOP

pUAS Sequences

FIGURE 3

1 ATGGCCAACAAGCTGAGGAAATCGAACGCCATCGAATGGGCCACGGCCACCGGCACAGTACCGCTCCTGGAAAGGAGCTGCTGCCACAGC
 1 M A N K L R K S N A I E W A T A T G T V P L L E R S C C H S

 91 GAGGACGCCGCACTGGAGCCCCAAGCGAGCAAAACCAGCCATAGAGAACAAGCCCCATCCTGCGCCACCTGAGCCAACTGAGCCACCTG TM
 31 E D A A L E P Q A S K T S H R E Q A P I L R H L S Q L S H L

 181 CTCATCATCGCCGACTGCTGATCGTCTGCTTGGCGGGCGTGACGGAGGGCCGCGGCATGCGCCGCTCATGTTGAGGAGTCCGACACG
 61 L I I A G L L I V C L A G V T E G R R H A P L M F E E S D T

 271 GGCAGGCGGTCCAACCGACCGCGTCAACGAATGCCAGTTTGGCAAAGTTTTCGCGCAATTGGGGTCCACCTGGTATGCGGATTGGGT
 91 G R R S N R P A V T E C Q F G K V L R E L G S T W Y A D L G

 361 CCACCCCTTCGGAGTTATGTACTGCATCAAGTGTGAATGTGTGCGCATACCCAAGAAGCGGCGCATCGTTCACGCGTCCAGTGTGCGAAT
 121 P P F G V M Y C I K C E C V A I P K K R R I V A R V Q C R N CR1

 451 ATCABAAAACGAGTGGCCGCGGCCAAATGCGATGATCCCATCTCGTTGCCGGAATGCTGCAAGACCTGTCCCGGCGATCGAAACGAT
 151 I K N E C P P A K C D D P I S L P G K C C K T C P G D R N D

 541 ACGGATGTAGCCTTGGATGTGCCCCGTGCCCAATGAAGAGGAAGAGCGCAACATGAAACATTACGCTGCGTTGCTAACGGGCCGACCTCC
 181 T D V A L D V P V P N E E E E R N M K H Y A A L L T G R T S
 *
 631 TATTTCTCAAGGGTGAGGAAATGAAGTCCATGTACACCACCTACAATCCGCAGAATCTGGTGGCCACCGCCCGTTTCTGTTCACAAG
 211 Y F L K G E E M K S M Y T T Y N P Q N V V A T A R F L F H K

 721 AAGAATCTATACTACTCTTCTACACCTCATCGCAATCGGTGCGTCCGCGTGCCATTCAATTGTTGATGATGCGGGTGTAATCCTGGAG
 241 K N L Y Y S F Y T S S R I G R P R A I Q F V D D A G V I L E

 811 GAGCATCAACTGGAGACCACCTTGGCGGGCACTCTCAGTGTCTATCAGAATGCCACGGGCAAGATCGGCCGCGGCTCGAGGCAGCGCGGC
 271 E H Q L E T T L A G T L S V Y A N A T G K I G R G S R N R G pUAS/PCR
 * * *
 901 CGCATCTTTTACCCATACGATGTTCTGACTATGCGGGCTATCCCTATCACGTCCCGGACTATGCACGATCCTATCCATATGACCTTCCA
 301 R I F Y P Y D V F D Y A G Y P Y D V P D Y A G S Y P Y D V P SX-HA

 991 GATTACGCTGCTCAGTGGCGCGCGATTATACGACGACGACGACAAATCA
 331 D Y A A N C G R D Y K D D D D K STOP IX-FLAG

FIGURE 4

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                                10           20           30           40           50           60           70
Nog protei MDHSQCLVTIIYALMVFLGLRIDQGQCQHYLHIRPAPSENLPVLDLIEHPDPIYDPKEKDNLNETLLRRTLMVGHFDP

SuperSog P                               260          270          280
[   71 ] _____ iqfvddagvile--EhqLetTlagTlsV--yqn
                                   ^^^^^^^^v^w^    ^_^^^_^^vv^^v^    ^^v
Nog protei VDLIEHPDPIYDPKEKDNLNETLLRRLTMVGHFDP
                                           . . . . .
                                           . . . . .
                                           . . . . .
                                90           100          110          120          130          140          150
                                *
Nog protei ILPEERLGVEDLGELDLLLRQKPSGAMPAEIKGLEFYEGLSKKHRLSKKLRRKLQMWLWSQTFCPVLYTWNDLG

SuperSog P                300            310 pUAS Vector
[   71 ] IgrgsRvpLEDLcEgtLLLw>
         ^v---^^v^^^v^v-^^^v
Nog protei ILPEERLGVEDLGELDLLLR

                                170          180          190          200          210          220
                                *
Nog protei RYVKVGCSCYSKRCSVP EGMVCKAAKS MHLTI LRWRRCORRVQQKC AWTIQYPVISECKC SC
```

FIGURE 5

-351 ATATTAGATGGACATGCATAATAATTATTCATGTAACATGTGATTTTCATTTTACACGAGGTGTAAGTCAGAATTTAAAATTCTTAAAA
 -261 ATTGCAATCACGGCTTATTGTACATATTTATGTATGCGATCTCATTATTATTATTATTATTATTGATAATATTAGCAGCTGTTCAAA
 -171 TCATCAACAAGTATAAAATTGAAAATGTTAAAAATTGAAGCAGTCTTGGGTTTGCTGCAACATGTTGCTGCCGATCGTTAGATGTTGCT

204 cDNA start

-81 GCTGCATGTTGCCGCTGCATGTTGCCGTTGCGCCGCTTGGGCACTTTATAAACACGAGCGGATTCAGTCTTTCAGGTTTCAG
 10 TCGCTCTGAATTGCGTGGGATTGCATCGGTGCTGCGCTTTTGGGTTTCGGCATTTAGAGAGATACGATACGATCCGATACGATCCG
 100 ATCCAGTACAAAAATCAAATTCAAACCGCACTCCCGATCCGGTCCGCATCATATACACGGCGGCTCGCACCGCAGCTATCTAGTAGATA
 190 AAAGTCGCCGAGAACGCGATACGCATATAGCGAAACGCCAAAAAATAAAAAAAGTCGCGTGTCTTAATCCCTCTCATACGAGAT
 280 CGACTCTATTTTCCAGAGCAAGCTAAACACACTAGTGCTAAACCATACTATATATCTAACTAAGGAAACAAAGTCTCGAAACTGAAAA
 370 CGAAAAGCGCAAATTTATGCGACGCTAAATAAAAAACAGAAACCAAAACATAAAACACACTATACAAATCATACAAAAACAAACAGCGA
 460 ATCAAATAGTATAAAAAAATAAATAAATGAGGAATAAAAAACAGGCAATAGAAATAAAATCCAATAAATCGGCGCGCGAACTCGCG
 550 TGTGTTATCTAATCTGCAAGAGAAGTACAAGAATCGGGTATAGAATCGGCTCTATACTATATCTATACACCTGATATATCTATATCCATT
 640 GTGTGTGCCAGTGTGTGCGTGGCGACCTTTGTTTTATATATTTTGTGTTGTTTCATACTGTGAAACGTGCTTTTACAAGCCGGTCG
 730 TTCAAAATACAAATACTACAAATCAAATCAAATCATATACATATATCAGTAAAAACAAAAACAAACACATACAACTGGCCAAC
 1 M A N

820 AAGCTGAGGAAATCGAACGCCATCGAATGGGCCACGGCCACCGGCACAGTACCGCTCCTGGAAAGGAGCTGTGCCACAGCGAGGACGCC
 4 K L R K S N A I E W A T A T G T V P L L E R S C C H S E D A

910 GCACTGGAGCCCAAGCGAGCAAAACCAGCCATAGAGAACAAGCCCCATCCTGCGCCACCTGAGCCAACTGAGCCACCTGCTCATCATC TM
 34 A L E P Q A S K T S H R E Q A P I L R H L S Q L S H L L I I

1000 GCGGACTGCTGATCGTCTGCTTGGCGGGCGTGACGAGGGGCCCGCGCATGCGCGCTCATGTTTCGAGGAGTCCGACACGGGCAGGCGG
 64 A G L L I V C L A G V T E G R R H A P L M F E E S D T G R R

1090 TCCAACCGACGAGCGGTTCACCGAATGCCAGTTTGGCAAAGTTTTCGCGCAATTGGGGTCCACCTGGTATGCGGATTGGGTCCACCTTC
 94 S N R P A V T E C Q F G K V L R E L G S T W Y A D L G P P F

1180 GGAGTTATGTACTGCATCAAGTGTGAATGTGTGGCGATACCCAAGAAGCGGCGCATCGTTGCACGCGTCCAGTGTGCGAATATCAAAAC
 124 G V M Y C I K C E C V A I P K K R R I V A R V Q C R N I K N

1270 GAGTGCCCGCGGCCAAATGCGATGATCCCATCTCGTTGCCCGGAAAATGCTGCAAGACCTGTCCCGCGATCGAAACGATACGGATGA
 154 E C P P A K C D D P I S L P G K C C K I C P G D R N D T D V

1360 GCCTTGGATGTGCCGTTGCCCAATGAAGAGGAAGAGCGCAACATGAAACATTACGCTGCGTTGCTAACGGGCGCACCTCTATTCTCTC
 184 A L D V P V P N E E E E R N M K H Y A A L L T G R T S Y F L

1450 AAGGGTGAGGAAATGAAGTCCATGTACACCACCTACAATCCGAGAATGTGGTGGCCACCGCCGTTTCTGTTCCACAAGAAGAATCTA
 214 K G E E M K S M Y T T Y N P Q N V V A T A R F L F H K K N L

1540 TACTACTCTTCTACACCTCATCGGAATCGGTGCTCCGCGTGCCTTCAATTGTTGATGATGCGGGTGTAACTCTGGAGGAGCATCAA
 244 Y Y S F Y T S S R I G R P R A I Q F V D D A G V I L E E H Q

1630 CTGGAGACCACCTTGGCGGGCACTCTCAGTGTCTATCAGAATGCCACGGGCAAGATCTGCGGTGTCTGGCGACGAGTTCACGTGATTAC
 274 L E T T L A G T L S V Y Q N A T G K I C G V W R R V P R D Y

1720 AAGCGCATCCTGCGCGACGATCGTCTCCATGTTGTCTCTCTCTGCGGCAACAAACAGCAGGCGGAGTTGGCTCTGGCCGAAAGGTGGCC
 304 K R I L R D D R L H V V L L W G N K Q Q A E L A L A G K V A

1810 AAATACACGGCCCTGCGAGCGGAGTTGTTTCAGTTTCGCTACTGGAGGCACCACTTCCCGATGGCAAAACGGATCCCCAGCTGGCCGGAGCC
 334 K Y T A L Q T E L F S S L L E A P L P D G K T D P Q L A G A

1900 GGTGGCACAGCGATCGTGTCCACGACGCGGTGCCGCTCATCGATGCATCTCACCTGGTCTTCAATGGTGTCTTTGGTGGCGAGGAG
 364 G G T A I V S T S S G A A S S M H L T L V F N G V F G A E E

1990 TACGCCGATGCAGCACTGAGTGTGAAAATTGAGCTGGCAGAACGGAAGGAGGTGATCTTCGATGAGATTCCACGTGTGCGCAAACCTCT
 394 Y A D A A L S V K I E L A E R K E V I F D E I P R V R K P S

2080 GCCGAGATCAATGTCCTGGAGCTGTCGTGCGCCATTTCCATACAGAATCTTCGACTGATGTGCGGTGGCAAACTCTGCTGACCGTGGAG
 424 A E I N V L E L S S P I S I Q N L R L M S R G K L L L T V E

2170 TCCAAGAAGTACCCACATCTGCGCATCCAGGGACACATCGTGACCCGAGCCAGCTGCGAAATCTTCCAGACCTGCTGGCGCCGACAGT
 454 S K K Y P H L R I Q G H I V T R A S C E I F Q T L L A P H S

2260 GCCGAATCTCGACCAAGAGCAGCGGTTTGGCGTGGGTCTACTTGAACACCGATGGATCTCTGGCCTACACATCGAAACGAGACGCTG
 484 A E S S T K S S G L A W V Y L N T D G S L A Y N I E T E H V

2350 AACACCCGGGATAGGCCCAACATCAGTTTGATTGAGGAGCAGGGCAAGCGGAAGGCCAAGCTGGAGGATCTGACGCCGAGCTTCAACTTC
 514 N T R D R P N I S L I E E Q G K R K A K L E D L T P S F N F

2440 AACCAGGCCATTGTTAGTGTGGAGAAGTTGGGTCCCAAGGTCCTCGAGTCGCTGTATGCCGGCGAACTGGGCGTTAATGTGGCCACCGAG
 544 N Q A I G S V E K L G P K V L E S L Y A G E L G V N V A T E

CR1

SR1

FIGURE 6

